IN THE SPECIFICATION:

Please amend the title to read "METHOD FOR ~~DETERMINING~~ SCREENING THE ALLELIC STATE [[OF]] AT THE 5'-[[END]]FLANKING REGION OF THE [[SG(A)S1-]] αS1 CASEIN GENE"

Page 2, please amend the paragraph beginning on line 11 as follows:

Regarding cattle and other species bred for milk production, the crucial criteria are the milk quantity, the protein content and fat. For these criteria, different QTL were identified, among other locations on the chromosome BTA 6. The potential QTL regions for protein contents are indicated relatively uniformly from different working groups within the area around or between the micro satellite markers *BM143* and *TGLA37* and thus approximately 20-30 centimorgans (cM) away from the casein locus (Spelman et al. 1996, *Genetics* 144, 1799-1808; Georges et al. 1995, *Genetics* 139, 907-920; ~~Boldly~~ Kühn et al. 1996, *J Anim Breed Genet* 133, 355-362; Zhang et al. 1998, *Genetics* 149, 1959-1973). According to Nadesalingam et al. (2001, *Mammalian Genome* 12, 27-31) the casein genes are, however, as well excluded as candidates for the observed QTL effects due to their position (40cM away from the QTL).

Page 3, please amend the paragraph beginning on line 18 as follows:

Various tests are described concerning the molecular genetic differentiation of the αs1 casein variants B and C (David & Deutch 1992, *Animal Genetics* 23, 425-429; Schlee & Rottmann 1992, *J Anim Breed Genet* 109, 316-319). Individual gene test procedures for the rare alleles A, D and F also exist, (Prinzenberg 1998, ISBN 3-922306-68-3; chapter 4.1, p. 61-71), as well as for the proof of a quantitative variant

of the αs1 casein G (Mariani et al 1995, *L'industria del Latte* 31, 3-13). By means of sequencing around 1,000 base pairs (bp) from the 5'-region of the αs1 casein gene from various cattle breeds, Schild & Geldermann (1996) showed 17 variable positions in the 5'-flanking region of the *CSN1S1* gene, of which 5 have been detected due to different recognition sequences for the restriction endonucleases with Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP). According to Ehrmann et al. (1997, *J Animal Breed Genet* 114, 121-132), the 5'-flanking variants are each linked with certain protein alleles, in such a manner that the existence of given protein variants implies the existence of certain variants in the 5'-flanking region. Koczan et al. (1993, *Animal Genetics* 24, 74) also described a gene test to discriminate the αs1 casein B against C in German American Holstein, Black and White, and Jersey cows which is based on a fragment from the 5'-flanking region of the αs1 casein. For the last test mentioned, the strict linkage with the protein mutations αs1 casein B and C has however in the meantime been refuted and therewith, the validity for the following breeds: Aberdeen Angus, Anatolian black, Angeln, Asturian Valley, Ayrshire, British Frisian, Casta Navarra, Charolais, Chianina, Fighting Bull, Hereford, Jersey, Maremmana, Pezzata Rossa, Piedmontese, Scottish Highland, Turkish Grey Steppe (Jann et al., [[2001]] 2002; *Arch. Tierz, Dummerstorf* 45, 13-21).

Page 8, please amend the paragraph beginning on line 26 as follows:

The four alleles were cloned and sequenced. The sequence analysis was in accordance with the sequence published by Koczan et al. (1991, Nucleic Acids Research 19, 5591-[[56596]]5596; Genbank Acc. No. X59856) for allele 2, except for the length of poly-T (from position 390 of figure 1 onwards). The alleles 1, 3 and 4

differ from this sequence by various substitutions and deletions. The variable positions are highlighted in the sequence alignment (figure 2). In alleles 1 and 4, potential transcription factor-binding sites are each affected by mutations. Thus, in allele 1, two potential binding sites (for AP-1 and YY1) cease to exist, whereas in allele 4, a new potential ABF1-binding site emerges.

Page 11, please amend the paragraph beginning on line 27 as follows:

In order to determine the allelic state, various standard techniques are available which are well known by the expert: The sequencing according to Sanger et al. 1977, through an illustration of single-strand conformation polymorphisms (SSCP, Orita et al. 1989, *Genomics* 5, 874-879), restriction fragment length polymorphisms (RFLP; Botstein et al. 1980, *American Journal of Human Genetics* 32, 314-331) and PCR-RFLP (Damiani et al. 1990, *Animal Genetics* 21, 107-114; Medrano & Aguilar-Cordova 1990, *Animal Biotechnology* 1,73-77), allele-specific PCR (= ARMS, ASPCR, PASA; Newton et al. 1989, *Nucleic Acids Research* 17, 2503-2516; [[Sakar]] Sarkar et al. 1990, *Analytical Biochemistry* 186, 64-68; David & Deutch 1992, *Animal Genetics* 23, 425-429), oligonucleotide-ligation assay (= OLA; Beck et al. 2002, *J Clinical Mikrobiol* 40, 1413-1419), temperature gradient gel electrophoresis (= TGGE, Tee et al. 1992, *Animal Genetics* 23, 431-435) and analogical procedures belonging to the technical state of the art.